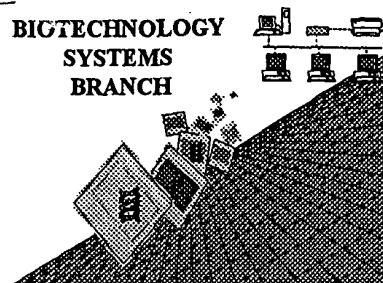


A. Mehta

# **RAW SEQUENCE LISTING** **ERROR REPORT**

BIGTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/180,798  
Art Unit / Team No. : 1649  
Date Processed by STIC: 1/13/2000

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**MARK SPENCER 703-308-4212**

# Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/180798

## ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
                                 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
                                 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
                                 This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                                 <400> sequence id number  
                                 000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

0. mehta

1649

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/180,798

DATE: 01/13/2000  
TIME: 12:18:42

Input Set: I180798.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

Does Not Comply  
Corrected Diskette Needed

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2 <120> TITLE OF INVENTION: Improvements in or relating to organic compounds  
3 <130> FILE REFERENCE: Jen1  
4 <140> CURRENT APPLICATION NUMBER: US/09/180,798  
5 <141> CURRENT FILING DATE: 1998-11-16  
6 <160> NUMBER OF SEQ ID NOS: 33  
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pp 1-2

see item 10 on Eva summary sheet

PAGE: 2

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/180,798DATE: 01/13/2000  
TIME: 12:18:42

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/180,798

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PAGE: 4

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/180,798

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TIME: 12:18:42

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/180,798

DATE: 01/13/2000  
TIME: 12:18:42

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215	250 255 260	
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223	Thr Pro Thr Glu Arg Leu Leu Val Tyr Pro Tyr Met Ala Asn Gly Ser	
224	300 305 310	
225	gtt gcg tcg tgt tta aga gag cgt cag cca tca gaa cct ccc ctt gat	1074
226	Val Ala Ser Cys Leu Arg Glu Arg Gln Pro Ser Glu Pro Pro Leu Asp	
227	315 320 325	
228	tggt cca act agg aag agg att gca cta gga tct gct agg ggg ctt tct	1122
229	Trp Pro Thr Arg Lys Arg Ile Ala Leu Gly Ser Ala Arg Gly Leu Ser	
230	330 335 340	
231	tat ttg cat gac cat tgt gat ccc aag att atc cat cgt gat gta aaa	1170
232	Tyr Leu His Asp His Cys Asp Pro Lys Ile Ile His Arg Asp Val Lys	
233	345 350 355	
234	gct gca aat ata tta ttg gac gaa gaa ttt gag gct gtt gta ggt gat	1218
235	Ala Ala Asn Ile Leu Leu Asp Glu Glu Phe Glu Ala Val Val Gly Asp	
236	360 365 370 375	
237	ttt ggg tta gct agg ctc atg gat tac aag gat acc cat gtt aca act	1266
238	Phe Gly Leu Ala Arg Leu Met Asp Tyr Lys Asp Thr His Val Thr Thr	
239	380 385 390	
240	gct gta agg ggt acc ttg ggc tac ata gct ccc gag tac ctc tcg act	1314
241	Ala Val Arg Gly Thr Leu Gly Tyr Ile Ala Pro Glu Tyr Leu Ser Thr	
242	395 400 405	
243	gga aag tca tca gag aag acc gat gtc ttt ggt tat ggg att atg ctc	1362
244	Gly Lys Ser Ser Glu Lys Thr Asp Val Phe Gly Tyr Gly Ile Met Leu	

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VERIFICATION SUMMARY  
PATENT APPLICATION US/09/180,798

DATE: 01/13/2000  
TIME: 12:18:42

Input Set: I180798.RAW

Line	? Error/Warning	Original Text
44	W "N" or "Xaa" used: Feature required	tctagatgac gaaatcgcg tacctttgat ttngaaat
55	W "N" or "Xaa" used: Feature required	acctgnggac aaaagaagcg ctgatgaact gatttaat
76	W "N" or "Xaa" used: Feature required	agtcacatna taaaattggn gggttgaca aatataac
272	W Invalid/Missing Amino Acid Numbering	